

(2)

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RAW SEQUENCE LISTING

DATE: 07/26/2001

PATENT APPLICATION: US/09/903,771

TIME: 15:20:52

Input Set : A:\203975US0X.txt

Output Set: N:\CRF3\07262001\I903771.raw

ENTERED

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3 <110> APPLICANT: MOCKEL, Bettina
4     KREUTZER, Caroline
5     BATHE, Brigitte
7 <120> TITLE OF INVENTION: NUCLEOTIDE SEQUENCES CODING FOR THE luxR GENE
9 <130> FILE REFERENCE: 203975US0X
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/903,771
C--> 11 <141> CURRENT FILING DATE: 2001-07-13
11 <150> PRIOR APPLICATION NUMBER: DE10039043.9
12 <151> PRIOR FILING DATE: 2000-08-10
14 <160> NUMBER OF SEQ ID NOS: 5
16 <170> SOFTWARE: PatentIn version 3.1
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 1052
20 <212> TYPE: DNA
21 <213> ORGANISM: Corynebacterium glutamicum
23 <220> FEATURE:
24 <221> NAME/KEY: CDS
25 <222> LOCATION: (214)..(849)
26 <223> OTHER INFORMATION:
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30 tgcagcattg ccggtggagc caccagaggg gtttgtcggg gcgcgggttt tggcagattc      60
32 ggactcaagt gctacaggcg aggttgaact aagttctcca actgacgatg agtaaggcta      120
34 gactaaagta cgattcatct gctcatcgat actcttgaag gcgcattttc attcgaaacg      180
36 aagtgcgcca ttgggaagga cctagttcaa aca atg att cgc gtg ctg ctt gct      234
37                               Met Ile Arg Val Leu Leu Ala
38                               1               5
40 gat gac cac gaa atc gtg agg ctc gga ctc cga gct gtg ctg gaa agc      282
41 Asp Asp His Glu Ile Val Arg Leu Gly Leu Arg Ala Val Leu Glu Ser
42      10               15               20
44 gcc gag gac att gaa gtg gtg ggc gaa gtc tcc acc gcc gaa ggt gcg      330
45 Ala Glu Asp Ile Glu Val Val Gly Glu Val Ser Thr Ala Glu Gly Ala
46      25               30               35
48 gtg cag gca gcc caa gaa ggc gga atc gac gtc atc ttg atg gac ctc      378
49 Val Gln Ala Ala Gln Glu Gly Gly Ile Asp Val Ile Leu Met Asp Leu
50 40               45               50               55
52 cga ttc ggc ccc ggc gtc caa gga acc cag gtt tcc aca ggc gca gac      426
53 Arg Phe Gly Pro Gly Val Gln Gly Thr Gln Val Ser Thr Gly Ala Asp
54      60               65               70
56 gcc acc gca gcc atc aag cga aac atc gat aac ccg cca aaa gtc ctg      474
57 Ala Thr Ala Ala Ile Lys Arg Asn Ile Asp Asn Pro Pro Lys Val Leu
58      75               80               85
60 gtc gtg acc aac tac gac acc gac aca gac atc ctc ggc gca atc gaa      522
61 Val Val Thr Asn Tyr Asp Thr Asp Thr Asp Ile Leu Gly Ala Ile Glu
62      90               95               100
64 gcc ggc gca ctg ggc tac ctg ctc aaa gac gcc cca ccg agc gaa ctc      570
65 Ala Gly Ala Leu Gly Tyr Leu Leu Lys Asp Ala Pro Pro Ser Glu Leu
66      105               110               115

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68 ctg gca gca gta cga tcc gca gca gaa ggt gac tcc aca ctg tca ccc 618
69 Leu Ala Ala Val Arg Ser Ala Ala Glu Gly Asp Ser Thr Leu Ser Pro
70 120 125 130 135
72 atg gtt gcg aac cgc ctg atg act cgc gtg cgc acc ccc aaa acc tca 666
73 Met Val Ala Asn Arg Leu Met Thr Arg Val Arg Thr Pro Lys Thr Ser
74 140 145 150
76 ctc acc cca cgt gaa ctg gaa gtt ctc aag ctg gtt gcc ggt gga tcc 714
77 Leu Thr Pro Arg Glu Leu Glu Val Leu Lys Leu Val Ala Gly Gly Ser
78 155 160 165
80 tcc aac cgc gac att ggc cgt atc ctc ttc ctc tca gaa gcc acg gtg 762
81 Ser Asn Arg Asp Ile Gly Arg Ile Leu Phe Leu Ser Glu Ala Thr Val
82 170 175 180
84 aaa tcc cac ctc gtg cac atc tac gac aag ctc ggc gtg cgg tca cgt 810
85 Lys Ser His Leu Val His Ile Tyr Asp Lys Leu Gly Val Arg Ser Arg
86 185 190 195
88 acc tcc gct gtc gca gcc gca cgt gag cag ggg ctg ctg tagcgggggt 859
89 Thr Ser Ala Val Ala Ala Arg Glu Gln Gly Leu Leu
90 200 205 210
92 tgctgcaagg ctttaggtat ccgcgccggg gttggcctac gggagcatcc cgaggcttta 919
94 gcaggggcac gggctctggc ttgggctgag tcagggggcgc ggccaatgct ttccgacgcg 979
96 tgtctccacg gctttattta gtttttcaag aagtttgacg aaggtgcgta gatcctcttc 1039
98 gggccagtct gaa 1052
101 <210> SEQ ID NO: 2
102 <211> LENGTH: 212
103 <212> TYPE: PRT
104 <213> ORGANISM: Corynebacterium glutamicum
106 <400> SEQUENCE: 2
108 Met Ile Arg Val Leu Leu Ala Asp Asp His Glu Ile Val Arg Leu Gly
109 1 5 10 15
112 Leu Arg Ala Val Leu Glu Ser Ala Glu Asp Ile Glu Val Val Gly Glu
113 20 25 30
116 Val Ser Thr Ala Glu Gly Ala Val Gln Ala Ala Gln Glu Gly Gly Ile
117 35 40 45
120 Asp Val Ile Leu Met Asp Leu Arg Phe Gly Pro Gly Val Gln Gly Thr
121 50 55 60
124 Gln Val Ser Thr Gly Ala Asp Ala Thr Ala Ala Ile Lys Arg Asn Ile
125 65 70 75 80
128 Asp Asn Pro Pro Lys Val Leu Val Val Thr Asn Tyr Asp Thr Asp Thr
129 85 90 95
132 Asp Ile Leu Gly Ala Ile Glu Ala Gly Ala Leu Gly Tyr Leu Leu Lys
133 100 105 110
136 Asp Ala Pro Pro Ser Glu Leu Leu Ala Ala Val Arg Ser Ala Ala Glu
137 115 120 125
140 Gly Asp Ser Thr Leu Ser Pro Met Val Ala Asn Arg Leu Met Thr Arg
141 130 135 140
144 Val Arg Thr Pro Lys Thr Ser Leu Thr Pro Arg Glu Leu Glu Val Leu
145 145 150 155 160
148 Lys Leu Val Ala Gly Ser Ser Asn Arg Asp Ile Gly Arg Ile Leu
149 165 170 175

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152 Phe Leu Ser Glu Ala Thr Val Lys Ser His Leu Val His Ile Tyr Asp
153          180          185          190
156 Lys Leu Gly Val Arg Ser Arg Thr Ser Ala Val Ala Ala Arg Glu
157          195          200          205
160 Gln Gly Leu Leu
161          210
164 <210> SEQ ID NO: 3
165 <211> LENGTH: 353
166 <212> TYPE: DNA
167 <213> ORGANISM: Corynebacterium glutamicum
169 <400> SEQUENCE: 3
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172 tccacaggcg cagacgccac cgcagccatc aagcgaaaca tcgataacct gccaaaagtc    120
174 ctgggtcgtg ccaactacga caccgacaca gacatcctcg gcgcaatcga agccggcgca    180
176 ctgggtctacc tgctcaaaga cgccccaccg agcgaactcc tggcagcagt acgatccgca    240
178 gcagaagggtg actccacact gtcacccatg gttgcgaacc gcctgatgac tcgcgtgcgc    300
180 acccccacaaa cctcactcac cccacgtgaa ctggaagtgc tcaagctggt tgc          353
183 <210> SEQ ID NO: 4
184 <211> LENGTH: 20
185 <212> TYPE: DNA
186 <213> ORGANISM: Corynebacterium glutamicum
188 <400> SEQUENCE: 4
189 ggaatcgacg tcattttgat                                20
192 <210> SEQ ID NO: 5
193 <211> LENGTH: 20
194 <212> TYPE: DNA
195 <213> ORGANISM: Corynebacterium glutamicum
197 <400> SEQUENCE: 5
198 gcaaccagct tgagaacttc                                20

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VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date